REMARKS

No claims have been canceled or amended in this paper. New claim 52 has been added in this paper. Therefore, claims 1-52 are pending. Of these claims, claims 1-38, 43-47 and 49-51 are withdrawn as being directed at a non-elected invention or non-elected species. Consequently, claims 39-42, 48 and 52 are under active consideration.

In the outstanding Office Action, the Patent Office communicates the following election of invention requirement:

> Restriction is required under 35 U.S.C. 121 and 372.
>
> This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1.
>
> In accordance with 37 CFR 1.499, applicant is required, in reply to this action, to elect a single invention to which the claims must be restricted.
>
> Group I, claim(s) 1-38, drawn to a method for amplification of nucleic acids.
>
> Group II, claim(s), 39-51, drawn to a method for designing primers.

In response to the above, Applicants respectfully elect Group II, claims 39-51.

Also, in the outstanding Office Action, the Patent Office communicates, in pertinent part, the following election of species requirement:

> This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.
>
> The species are as follows:
>
> a. Species of nature of primer (claim 1 is generic)

i. primer molecules do not contain nucleic acid sequences complementary or identical to nucleic acid sequences of the target sequence which prior to treatment fo step 2 contained a 5'-CG-3' site (claim 2).
ii. primer molecule comprises of at least one nucleotide within the last three nucleotides from the 3' end of the molecule wherein said nucleotide is complementary to a nucleotide of the target sequence that was converted to a different nucleotide by the treatment performed in step 2) of claim 1 (claim 11).
iii. Primer molecule comprises of at least one nucleotide within the last three nucleotides from the 3' end of the molecule wherein said nucleotide is complementary to a nucleotide of the target sequence that was converted to a different nucleotide by bisulfite treatment (claim 12).
iv. primer molecule is characterized in that the last at least 5 bases at the 3'end of said primer molecule are not complementary to the sequence of any other primer molecule in the set (claim 3).
v. Primer molecules are reaching a specified value of linguistic complexity (claim 5).
vi. Primer molecules are reaching a specified value of Shannon entropy (claim 6).
vii. Primer molecules are comprised of 16-50 nucleotides (claim 34).
viii. primer molecules do not form dimers with each other (claim 35).
ix. primer molecules do not form loops or hairpin structures (claim 36).
x. primer molecules are complementary to target (claim 37)

b. Species of nucleic acid sample (claim 1 is generic)
xi. ucleic acid sample is comprised of plasmid DNA, BACs, YACs or genomic DNA (claim 8)
xii. nucleic acid sample is comprised of human genomic DNA (claim 9)

c. Species of numbers of primer pairs in a set (claim 1 is generic)

xiii. set is comprised of at least one but not more than 32 primer pairs (claim 3).

xiv. set is comprised of at least one but not more than 16 primer pairs (claim 4).

d. Species of number of mismatches allowed (claim 1 is generic)

xv. number of mismatches allowed for when virtually testing the amplification of unwanted products according to step 3c) of claim 1 is less than 20% of the number of nucleotides of the primer molecule (claim 14).

xvi. number of mismatches allowed for when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is less than 10% of the number nucleotides of the primer molecule (claim 16).

xvii. number of mismatches allowed for when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is less than 5% of the number of nucleotides of the primer molecule (claim 18).

xviii. number of mismatches allowed for when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is less than seven (claim 20).

xix. number of mismatches allowed for is less than five (claim 21).

xx. number of mismatches allowed for is less than three (claim 22).

xxi. number of mismatches allowed for is one (claim 23).

xxii. number of mismatches allowed for when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is determined by a pre-specified maximum melting temperature (claim 24).

e. Species of number of nucleotides creating one gap allowed for in primer molecule (claim 1 is generic)

xxiii. the number of nucleotides creating one gap, when aligning the primer molecule sequence with the template sequence, allowed for, when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is

less than 20% of the number of molecules of the primer molecule (claim 15).

xxiv. the number of nucleotides creating one gap, when aligning the primer molecule sequence with the template sequence, allowed for, when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is less than 10% of the number of nucleotides of the primer molecule (claim 17).

xxv. number of nucleotides creating one gap, when aligning the primer molecule sequence with the template sequence, allowed for, when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is less than 5% of the number of nucleotides of the primer molecule (claim 19).

f. Species of nature of nucleic acid amplified by primer molecules (claim 1 is generic)

xxvi. nucleic acid sequences that prior to treatment of step 2 comprised of more than eight 5'-CG-3' sites (claim 25).

xxvii. nucleic acid sequences that prior to treatment of step 2 comprised of more than six 5'-CG-3' sites (claim 26).

xxviii. nucleic acid sequences that prior to treatment of step 2 comprised of more than four 5'-CG-3' sites (claim 27).

xxix. nucleic acid sequences that prior to treatment of step 2 comprised of more than two 5'-CG-3' sites (claim 28).

xxx. nucleic acids which are comprised of at least 50 bp but not more than 2000 bp (claim 32).

xxxi. nucleic acids which are comprised of at least 80 bp but not more than 1000 bp (claim 33).

xxxii. Primer molecules amplify regions of the treated nucleic acids which prior to treatment performed in step 2) of claim 1 did not contain specified restriction enzyme recognition sites (claim 38).

g. Species of virtual PCR (claim 1 is generic)

xxxiii. electronic PCR (claim 29)

xxxiv. electronic PCR, taking as template nucleic acid the coding strand of the treated sample,

the non-coding strand of the treated sample and both of the strands of the untreated sample (claim 30).

xxxv. electronic PCR, taking as template nucleic acid the coding strand of the bisulfite converted human genome, the non-coding strand of the bisulfite converted human genome and both of the strands of the untreated human genome (claim 31).

h. Species of measure of complexity (claim 39 is generic)

xxxvi. measure of complexity is a measure of linguistic complexity (claim 42).

xxxvii. measure of complexity is a measure of Shannon entropy (claim 43).

i. Species of step carried out prior to performing step d) (claim 39 is generic)

xxxviii. excluding from the remaining primer pairs those pairs, which consist of a primer molecule that comprises of at least one CpG site (claim 44).

xxxix. excluding from the remaining primer pairs those pairs, which consist of a primer molecule that does not contain at least one nucleotide within the last three nucleotides from the 3' end of the molecule wherein said nucleotide is complementary to a nucleotide of the target sequence that was converted to a different nucleotide by the treatment performed in step 2) (claim 45)

xl. excluding from the remaining primer pairs those pairs, which consist of a primer molecule that contains more than 5 bases at its 3' end that are complementary to any other primer molecule's sequence in the set (claim 46).

xli. excluding from the remaining primer pairs those pairs, which amplify a nucleic acid that did not, prior to the treatment in step 2 contain at least two CpG sites (claim 47).

xlii. excluding from the remaining primer pairs those pairs, which comprise of one primer molecule that in combination with another primer molecule in the set amplifies an

unwanted product, when virtually testing according to step 3 c) under conditions allowing for a number of mismatching nucleotides of 20% of the number of nucleotides of the primer molecule (claim 48).

xliii. excluding from the remaining primer pairs those pairs, which comprise of one primer molecule that in combination with another primer molecule in the set amplifies an unwanted product, when virtually testing according to step 3 c) under conditions allowing for a number of nucleotides creating one gap, when aligning the primer molecule sequence with the template sequence, of up to 20% of the number of nucleotides of the primer molecule (claim 49).

xliv. excluding from the remaining primer pairs those pairs, which comprise of one primer molecule that in combination with another primer molecule in the set amplifies an unwanted product, when virtually testing according to step 3c) under conditions allowing for four or less mismatching base pairs (claim 50).

xlv. excluding from the remaining primer pairs those pairs, which comprise of one primer molecule that in combination with another primer molecule in the set amplifies an unwanted product, when virtually testing according to step 3 c) under conditions allowing for two or less mismatching base pairs (claim 51).

Applicant is required, in reply to this action, to elect a single species from each of the categories a) through i) enumerated above to which the claims shall be restricted if no generic claim is finally held to be allowable. The reply must also identify the claims readable on the elected species, including any claims subsequently added. An argument that a claim is allowable or that all claims are generic is considered non-responsive unless accompanied by an election.

In response to the above, Applicants respectfully elect the following species: a. Species of nature of primer – i (primer molecules do not contain nucleic acid sequences complementary or identical to nucleic acid sequences of the target sequence which prior to treatment of step 2 contained a 5'-CG-3' site); b. Species of nucleic acid sample – xii (nucleic acid sample is comprised of human genomic DNA); c. Species of numbers of primer pairs in a set – xiii (set is comprised of at least one but not more than 32 primer pairs); d. Species of number of mismatches allowed – xxi (number of mismatches allowed for is one); e. Species of number of nucleotides creating one gap allowed for in primer molecule – xxv (number of nucleotides creating one gap, when aligning the primer molecule sequence with the template sequence, allowed for, when virtually testing the amplification of unwanted products according to step 3 c) of claim 1 is less than 5% of the number of nucleotides of the primer molecule); f. Species of nature of nucleic acid amplified by primer molecules - xxix (nucleic acid sequences that prior to treatment of step 2 comprised of more than two 5'-CG-3' sites); g. Species of virtual PCR – xxxv (electronic PRC, taking as template nucleic acid the coding strand of the bisulfite converted human genome, the non-coding strand of the bisulfite converted human genome and both of the strands of the untreated human genome); h. Species of measure of complexity – xxxvi (measure of complexity is a measure of linguistic complexity); and i. Species of step carried out prior to performing step d) – xlii (excluding from the remaining primer pairs those pairs, which comprise of one primer molecule that in combination with another primer molecule in the set amplifies an unwanted product, when virtually testing according to step 3 c) under conditions allowing for a number of mismatching nucleotides of 20% of the number of nucleotides of the primer molecule).

Claims 39-42, 48 and 52 are readable on the elected species.

In conclusion, it is respectfully submitted that the present application is in condition for allowance. Prompt and favorable action is earnestly solicited.

If there are any fees due in connection with the filing of this paper that are not accounted for, the Examiner is authorized to charge the fees to our Deposit Account No. 11-1755. If a fee is required for an extension of time under 37 C.F.R. 1.136 that is not accounted for already, such an extension of time is requested and the fee should also be charged to our Deposit Account.

Respectfully submitted,

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I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Mail Stop Amendment, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on February 19, 2008

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Edward M. Kriegsman